

RAW SEQUENCE LISTING

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Application Serial Number: 10/780, 043 A
Source: JFW/16
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IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/780,043A

DATE: 05/04/2006

TIME: 12:02:58

Input Set : A:\10-780,043.txt

Output Set: N:\CRF4\05042006\J780043A.raw

3 <110> APPLICANT: Bates, Elizabeth
 4 Fournier, Nathalie
 5 Chalus, Lionel
 6 Garrone, Pierre
 8 <120> TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND
 9 METHODS
 11 <130> FILE REFERENCE: SF0977XB
 13 <140> CURRENT APPLICATION NUMBER: US 10/780,043A
 14 <141> CURRENT FILING DATE: 2004-02-17
 16 <150> PRIOR APPLICATION NUMBER: US 09/869,388
 17 <151> PRIOR FILING DATE: 1999-12-29
 19 <150> PRIOR APPLICATION NUMBER: US 09/223,919
 20 <151> PRIOR FILING DATE: 1998-12-31
 22 <150> PRIOR APPLICATION NUMBER: US 09/224,604
 23 <151> PRIOR FILING DATE: 1998-12-31
 25 <160> NUMBER OF SEQ ID NOS: 16
 27 <170> SOFTWARE: PatentIn version 3.3
 29 <210> SEQ ID NO: 1
 30 <211> LENGTH: 1249
 31 <212> TYPE: DNA
 32 <213> ORGANISM: Homo sapiens
 35 <220> FEATURE:
 36 <221> NAME/KEY: CDS
 37 <222> LOCATION: (154)..(1062)
 39 <220> FEATURE:
 40 <221> NAME/KEY: sig_peptide
 41 <222> LOCATION: (154)..(210)
 43 <220> FEATURE:
 44 <221> NAME/KEY: mat_peptide
 45 <222> LOCATION: (211)..(1062)
 47 <400> SEQUENCE: 1

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52	tggtctcccc gtccccctgga gaagaacaag gcc atg ggt cgg ccc ctg ctg ctg	174
53	Met Gly Arg Pro Leu Leu Leu	
54	-15	
56	ccc cta ctg ccc ctg ctg ccg cca gca ttt ctg cag cct agt ggc	222
57	Pro Leu Leu Pro Leu Leu Leu Pro Pro Ala Phe Leu Gln Pro Ser Gly	
58	-10 -5 -1 1	
60	tcc aca gga tct ggt cca agc tac ctt tat ggg gtc act caa cca aaa	270
61	Ser Thr Gly Ser Gly Pro Ser Tyr Leu Tyr Gly Val Thr Gln Pro Lys	
62	5 10 15 20	
64	cac ctc tca gcc tcc atg ggt ggc tct gtg gaa atc ccc ttc tcc ttc	318

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65 His Leu Ser Ala Ser Met Gly Gly Ser Val Glu Ile Pro Phe Ser Phe		
66 25 30 35		
68 tat tac ccc tgg gag tta gcc aca gct ccc gac gtg aga ata tcc tgg	366	
69 Tyr Tyr Pro Trp Glu Leu Ala Thr Ala Pro Asp Val Arg Ile Ser Trp		
70 40 45 50		
72 aga cgg ggc cac ttc cac ggg cag tcc ttc tac agc aca agg ccg cct	414	
73 Arg Arg Gly His Phe His Gly Gln Ser Phe Tyr Ser Thr Arg Pro Pro		
74 55 60 65		
76 tcc att cac aag gat tat gtg aac cgg ctc ttt ctg aac tgg aca gag	462	
77 Ser Ile His Lys Asp Tyr Val Asn Arg Leu Phe Leu Asn Trp Thr Glu		
78 70 75 80		
80 ggt cag aag agc ggc ttc ctc agg atc tcc aac ctg cag aag cag gac	510	
81 Gly Gln Lys Ser Gly Phe Leu Arg Ile Ser Asn Leu Gln Lys Gln Asp		
82 85 90 95 100		
84 cag tct gtg tat ttc tgc cga gtt gag ctg gac aca cgg agc tca ggg	558	
85 Gln Ser Val Tyr Phe Cys Arg Val Glu Leu Asp Thr Arg Ser Ser Gly		
86 105 110 115		
88 agg cag cag tgg cag tcc atc gag ggg acc aaa ctc tcc atc acc cag	606	
89 Arg Gln Gln Trp Gln Ser Ile Glu Gly Thr Lys Leu Ser Ile Thr Gln		
90 120 125 130		
92 gct gtc acg acc acc cag agg ccc agc agc atg act acc acc tgg	654	
93 Ala Val Thr Thr Gln Arg Pro Ser Ser Met Thr Thr Thr Trp		
94 135 140 145		
96 agg ctc agt agc aca acc aca acc ggc ctc agg gtc aca cag ggc	702	
97 Arg Leu Ser Ser Thr Thr Thr Gly Leu Arg Val Thr Gln Gly		
98 150 155 160		
100 aaa cga cgc tca gac tct tgg cac ata agt ctg gag act gct gtg ggg	750	
101 Lys Arg Arg Ser Asp Ser Trp His Ile Ser Leu Glu Thr Ala Val Gly		
102 165 170 175 180		
104 gtg gca gtg gct act gtg ctc gga atc atg att ttg gga ctg atc	798	
105 Val Ala Val Ala Val Thr Val Leu Gly Ile Met Ile Leu Gly Leu Ile		
106 185 190 195		
108 tgc ctc ctc agg tgg agg aga agg aaa ggt cag cag cgg act aaa gcc	846	
109 Cys Leu Leu Arg Trp Arg Arg Lys Gly Gln Gln Arg Thr Lys Ala		
110 200 205 210		
112 aca acc cca gcc agg gaa ccc ttc caa aac aca gag gag cca tat gag	894	
113 Thr Thr Pro Ala Arg Glu Pro Phe Gln Asn Thr Glu Glu Pro Tyr Glu		
114 215 220 225		
116 aat atc agg aat gaa gga caa aat aca gat ccc aag cta aat ccc aag	942	
117 Asn Ile Arg Asn Glu Gly Gln Asn Thr Asp Pro Lys Leu Asn Pro Lys		
118 230 235 240		
120 gat gac ggc atc gta tat gct tcc ctt gcc ctc tcc agc tcc acc tca	990	
121 Asp Asp Gly Ile Val Tyr Ala Ser Leu Ala Leu Ser Ser Thr Ser		
122 245 250 255 260		
124 ccc aga gca cct ccc agc cac cgt ccc aag agc ccc cag aac gag	1038	
125 Pro Arg Ala Pro Pro Ser His Arg Pro Leu Lys Ser Pro Gln Asn Glu		
126 265 270 275		
128 acc ctg tac tct gtc tta aag gcc taaccaatgg acagccctct caagactgaa	1092	
129 Thr Leu Tyr Ser Val Leu Lys Ala		

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130 280
132 tggtagggcc aggtacagtgcgcacacct gtaatcccag ctactctgaa gcctgaggca 1152
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140 <211> LENGTH: 303
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144 <400> SEQUENCE: 2
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154 Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly Gly Ser
155 15 20 25
158 Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala Thr Ala
159 30 35 40 45
162 Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly Gln Ser
163 50 55 60
166 Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val Asn Arg
167 65 70 75
170 Leu Phe Leu Asn Trp Thr Glu Gly Gln Lys Ser Gly Phe Leu Arg Ile
171 80 85 90
174 Ser Asn Leu Gln Lys Gln Asp Gln Ser Val Tyr Phe Cys Arg Val Glu
175 95 100 105
178 Leu Asp Thr Arg Ser Ser Gly Arg Gln Gln Trp Gln Ser Ile Glu Gly
179 110 115 120 125
182 Thr Lys Leu Ser Ile Thr Gln Ala Val Thr Thr Thr Gln Arg Pro
183 130 135 140
186 Ser Ser Met Thr Thr Trp Arg Leu Ser Ser Thr Thr Thr Thr Thr
187 145 150 155
190 Gly Leu Arg Val Thr Gln Gly Lys Arg Arg Ser Asp Ser Trp His Ile
191 160 165 170
194 Ser Leu Glu Thr Ala Val Gly Val Ala Val Ala Val Thr Val Leu Gly
195 175 180 185
198 Ile Met Ile Leu Gly Leu Ile Cys Leu Leu Arg Trp Arg Arg Arg Lys
199 190 195 200 205
202 Gly Gln Gln Arg Thr Lys Ala Thr Thr Pro Ala Arg Glu Pro Phe Gln
203 210 215 220
206 Asn Thr Glu Glu Pro Tyr Glu Asn Ile Arg Asn Glu Gly Gln Asn Thr
207 225 230 235
210 Asp Pro Lys Leu Asn Pro Lys Asp Asp Gly Ile Val Tyr Ala Ser Leu
211 240 245 250
214 Ala Leu Ser Ser Ser Thr Ser Pro Arg Ala Pro Pro Ser His Arg Pro
215 255 260 265
218 Leu Lys Ser Pro Gln Asn Glu Thr Leu Tyr Ser Val Leu Lys Ala
219 270 275 280
222 <210> SEQ ID NO: 3
223 <211> LENGTH: 943

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224 <212> TYPE: DNA
225 <213> ORGANISM: Homo sapiens
228 <220> FEATURE:
229 <221> NAME/KEY: CDS
230 <222> LOCATION: (130)..(819)
232 <220> FEATURE:
233 <221> NAME/KEY: sig_peptide
234 <222> LOCATION: (130)..(180)
236 <220> FEATURE:
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238 <222> LOCATION: (181)..(819)
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243 ctcccacaggg cccctctctt gcctggacgg ctctgctggt ctccccgtcc cctggagaag 120
245 aacaaggccc atg ggt egg ccc ctg ctg ccc cta ctg ccc ctg ctg ctg ctg 171
246 Met Gly Arg Pro Leu Leu Leu Pro Leu Leu Pro Leu Leu Leu
247 -15. -10 -5
249 ccg cca gca ttt ctg cag cct agt ggc tcc aca gga tct ggt cca agc 219
250 Pro Pro Ala Phe Leu Gln Pro Ser Gly Ser Thr Gly Ser Gly Pro Ser
251 -1 T 5 10
253 tac ctt tat ggg gtc actcaa cca aaa cac ctc tca gcc tcc atg ggt 267
254 Tyr Leu Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly
255 15 20 25
257 ggc tct gtg gaa atc ccc ttc tcc ttc tat tac ccc tgg gag tta gcc 315
258 Gly Ser Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala
259 30 35 40 45
261 aca gct ccc gac gtg aga ata tcc tgg aga cgg ggc cac ttc cac ggg 363
262 Thr Ala Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly
263 50 55 60
265 cag tcc ttc tac agc aca agg ccc cct tcc att cac aag gat tat gtg 411
266 Gln Ser Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val
267 65 70 75
269 aac cgg ctc ttt ctg aac tgg aca gag ggt cag aag agc ggc ttc ctc 459
270 Asn Arg Leu Phe Leu Asn Trp Thr Glu Gly Gln Lys Ser Gly Phe Leu
271 80 85 90
273 agg atc tcc aac ctg cag aag cag gac cag tct gtg tat ttc tgc cga 507
274 Arg Ile Ser Asn Leu Gln Lys Gln Asp Gln Ser Val Tyr Phe Cys Arg
275 95 100 105
277 gtt gag ctg gac aca cgg agc tca ggg agg cag cag tgg cag tcc atc 555
278 Val Glu Leu Asp Thr Arg Ser Ser Gly Arg Gln Gln Trp Gln Ser Ile
279 110 115 120 125
281 gag ggg acc aaa ctc tcc atc acc cag ggt cag cag cgg act aaa gcc 603
282 Glu Gly Thr Lys Leu Ser Ile Thr Gln Gly Gln Gln Arg Thr Lys Ala
283 130 135 140
285 aca acc cca gcc agg gaa ccc ttc caa aac aca gag gag cca tat gag 651
286 Thr Thr Pro Ala Arg Glu Pro Phe Gln Asn Thr Glu Glu Pro Tyr Glu
287 145 150 155
289 aat atc agg aat gaa gga caa aat aca gat ccc aag cta aat ccc aag 699
290 Asn Ile Arg Asn Glu Gly Gln Asn Thr Asp Pro Lys Leu Asn Pro Lys

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291	160	165	170	
293	gat gac ggc atc gtc tat gct tcc ctt gcc ctc tcc agc tcc acc tca			747
294	Asp Asp Gly Ile Val Tyr Ala Ser Leu Ala Leu Ser Ser Ser Thr Ser			
295	175	180	185	
297	ccc aga gca cct ccc agc cac cgt ccc ctc aag agc ccc cag aac gag			795
298	Pro Arg Ala Pro Pro Ser His Arg Pro Leu Lys Ser Pro Gln Asn Glu			
299	190	195	200	205
301	acc ctg tac tct gtc tta aag gcc taaccaatgg acagccctct caagactgaa			849
302	Thr Leu Tyr Ser Val Leu Lys Ala			
303	210			
305	tggtgaggcc aggtacagtgcgcacacct gtaatcccag ctactctgaa gcctgaggca			909
307	gaatcaagtgcgcccaggatcaggcca gctt			943
310	<210> SEQ ID NO: 4			
311	<211> LENGTH: 230			
312	<212> TYPE: PRT			
313	<213> ORGANISM: Homo sapiens			
315	<400> SEQUENCE: 4			
317	Met Gly Arg Pro Leu Leu Leu Pro Leu Leu Pro Leu Leu Pro Pro			
318	-15	-10	-5	
321	Ala Phe Leu Gin Pro Ser Gly Ser Thr Gly Ser Gly Pro Ser Tyr Leu			
322	-1 1	5	10	15
325	Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly Gly Ser			
326	20	25	30	
329	Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala Thr Ala			
330	35	40	45	
333	Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly Gln Ser			
334	50	55	60	
337	Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val Asn Arg			
338	65	70	75	
341	Leu Phe Leu Asn Trp Thr Glu Gly Gln Lys Ser Gly Phe Leu Arg Ile			
342	80	85	90	95
345	Ser Asn Leu Gln Lys Gln Asp Gln Ser Val Tyr Phe Cys Arg Val Glu			
346	100	105	110	
349	Leu Asp Thr Arg Ser Ser Gly Arg Gln Gln Trp Gln Ser Ile Glu Gly			
350	115	120	125	
353	Thr Lys Leu Ser Ile Thr Gln Gly Gln Gln Arg Thr Lys Ala Thr Thr			
354	130	135	140	
357	Pro Ala Arg Glu Pro Phe Gln Asn Thr Glu Glu Pro Tyr Glu Asn Ile			
358	145	150	155	
361	Arg Asn Glu Gly Gln Asn Thr Asp Pro Lys Leu Asn Pro Lys Asp Asp			
362	160	165	170	175
365	Gly Ile Val Tyr Ala Ser Leu Ala Leu Ser Ser Ser Thr Ser Pro Arg			
366	180	185	190	
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374	210			
377	<210> SEQ ID NO: 5			
378	<211> LENGTH: 1450			

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/780,043A

DATE: 05/04/2006

TIME: 12:02:59

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